

1/18

SEQUENCE LISTING

<110> Chugai Seiyaku Kabushiki Kaisha  
<110> University College London  
<120> HM 1.24-UTILIZING CANCER VACCINES  
<130> M915  
<160> 23  
<210> 1  
<211> 109  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Synthetic DNA comprising leader sequence and HA coding  
sequence  
<400> 1  
aattccacc atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt 60  
ccactcatac ccatacgacg tccagacta cgctggtacc gcggccgcg 109  
<210> 2  
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<212> DNA  
<213> Artificial Sequence  
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<223> Synthetic DNA comprising leader sequence and HA coding  
sequence  
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gatccgcggc cgcggtacca gcgtagtctg ggacgtcgta tgggtatgag tggacacctg 60  
tagctgttgc taaccaagaag aggatgatac agtccatcc catggtggg 109  
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<223> Primer  
<400> 3

taaaggtacc aacagcgagg cctgccg

27

<210> 4

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 4

ctgctgcagt gagatcccag gatccata

28

<210> 5

<211> 396

<212> DNA

<213> Homosapiens

<223> Nucleotide sequence of extracellular domain of soluble  
HM 1.24 antigenic protein

<400> 5

aac agc gag gcc tgc cgg gac ggc ctt cgg gca gtg atg gag tgt cgc 48

Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg

1 5 10 15

aat gtc acc cat ctc ctg caa caa gag ctg acc gag gcc cag aag ggc 96

Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly

20 25 30

ttt cag gat gtg gag gcc cag gcc gcc acc tgc aac cac act gtg atg 144

Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met

35 40 45

gcc cta atg gct tcc ctg gat gca gag aag gcc caa gga caa aag aaa 192

Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys

50 55 60

gtg gag gag ctt gag gga gag atc act aca tta aac cat aag ctt cag 240

Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln

65 70 75 80

gac gcg tct gca gag gtg gag cga ctg aga aga gaa aac cag gtc tta 288

Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu  
                             85                            90                            95  
 agc gtg aga atc gcg gac aag aag tac tac ccc agc tcc cag gac tcc 336  
 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser  
                             100                            105                            110  
 agc tcc gct gcg gcg ccc cag ctg ctg att gtg ctg ctg ggc ctc agc 384  
 Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser  
                             115                            120                            125  
 gct ctg ctg cag 396  
 Ala Leu Leu Gln  
                             130  
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 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Primer  
 <400> 6  
 ataggatcct caagcggagc tggagtcctg 30  
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 <211> 345  
 <212> DNA  
 <213> Homosapiens  
 <223> Nucleotide sequence of extracellular domain of C-  
 terminal-lacking soluble HM 1.24 antigenic protein  
 <400> 7  
 aac agc gag gcc tgc cgg gac ggc ott cgg gca gtg atg gag tgt cgc 48  
 Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg  
                             1                            5                            10                            15  
 aat gtc acc cat ctc ctg caa caa gag ctg acc gag gcc cag aag ggc 96  
 Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly  
                             20                            25                            30  
 ttt cag gat gtg gag gcc cag gcc gcc acc tgc aac cac act gtg atg 144

Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met	
35 40 45	
gcc cta atg gct tcc ctg gat gca gag aag gcc caa gga caa aag aaa	192
Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys	
50 55 60	
gtg gag gag ctt gag gga gag atc act aca tta aac cat aag ctt cag	240
Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln	
65 70 75 80	
gac gcg tct gca gag gtg gag cga ctg aga aga gaa aac cag gtc tta	288
Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu	
85 90 95	
agc gtg aga atc gcg gac aag aag tac tac ccc agc tcc cag gac tcc	336
Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser	
100 105 110	
agc tcc gct	345
Ser Ser Ala	
115	
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<212> DNA	
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<220>	
<223> Primer	
<400> 8	
ggatcttggt tcattctcaa gcctcagaca gt	32
<210> 9	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 9	
cctcagactc ggctgaccc gtggaaagaa	30

&lt;210&gt; 10

&lt;211&gt; 429

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Nucleotide sequence coding for a fusion protein  
comprising HA peptide and soluble HM 1.24 antigenic protein

&lt;400&gt; 10

tac cca tac gac gtc cca gac tac gct ggt acc aac agc gag gcc tgc	48
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys	
1 5 10 15	
cgg gac ggc ctt cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc	96
Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu	
20 25 30	
ctg caa caa gag ctg acc gag gcc cag aag ggc ttt cag gat gtg gag	144
Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu	
35 40 45	
gcc cag gcc gcc acc tgc aac cac act gtg atg gcc cta atg gct tcc	192
Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser	
50 55 60	
ctg gat gca gag aag gcc caa gga caa aag aaa gtg gag gag ctt gag	240
Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu	
65 70 75 80	
gga gag atc act aca tta aac cat aag ctt cag gac gcg tct gca gag	288
Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu	
85 90 95	
gtg gag cga ctg aga aga gaa aac cag gtc tta agc gtg aga atc gcg	336
Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala	
100 105 110	
gac aag aag tac tac ccc agc tcc cag gac tcc agc tcc gct gcg gcg	384
Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala	
115 120 125	
ccc cag ctg ctg att gtg ctg ctg ggc ctc agc gct ctg ctg cag	429

Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln

130

135

140

<210> 11

<211> 378

<212> DNA

<213> Artificial Sequence

<223> Nucleotide sequence coding for a fusion protein  
comprising HA peptide and C-terminal- lacking soluble HM 1.24  
antigenic protein

<400> 11

tac cca tac gac gtc cca gac tac gct ggt acc aac agc gag gcc tgc	48
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys	
1 5 10 15	
cgg gac ggc ctt cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc	96
Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu	
20 25 30	
ctg caa caa gag ctg acc gag gcc cag aag ggc ttt cag gat gtg gag	144
Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu	
35 40 45	
gcc cag gcc gcc acc tgc aac cac act gtg atg gcc cta atg gct tcc	192
Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser	
50 55 60	
ctg gat gca gag aag gcc caa gga caa aag aaa gtg gag gag ctt gag	240
Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu	
65 70 75 80	
gga gag atc act aca tta aac cat aag ctt cag gac gcg tct gca gag	288
Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu	
85 90 95	
gtg gag cga ctg aga aga gaa aac cag gtc tta agc gtg aga atc gcg	336
Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala	
100 105 110	
gac aag aag tac tac ccc agc tcc cag gac tcc agc tcc gct	378

Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala

115

120

125

<210> 12

<211> 379

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence coding for L chain V region version  
a of humamized anti-HM 1.24 antibady

<400> 12

atg gga tgg agc tgt atc atc ctc tcc ttg gta gca aca gct aca ggt 48

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly

-15

-10

-5

gtc cac tcc gac atc cag atg acc cag agc cca agc agc ctg agc gcc 96

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala

-1 1

5

10

agc gtg ggt gac aga gtg acc atc acc tgt aag gct agt cag gat gtg 144

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val

15

20

25

aat act gct gta gcc tgg tac cag cag aag cca gga aag gct cca aag 192

Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys

30

35

40

45

ctg ctg atc tac tcg gca tcc aac cgg tac act ggt gtg cca agc aga 240

Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg

50

55

60

ttc agc ggt agc ggt agc ggt acc gac ttc acc ttc acc atc agc agc 288

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser

65

70

75

ctc cag cca gag gac atc gct acc tac tac tgc cag caa cat tat agt 336

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser

80

85

90

act cca ttc acg ttc ggc caa ggg acc aag gtg gaa atc aaa c 379

Thr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

95

100

105

<210> 13

<211> 418

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence coding for H chain V region version  
r of humanized anti-HM 1.24 antibody

<400> 13

atg gac tgg acc tgg agg gtc ttc ttc ttg ctg gct gta gct cca ggt 48

Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly

-15

-10

-5

gct cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 96

Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys

-1 1

5

10

cct ggg gcc tca gtg aag gtt tcc tgc aag gca tct gga tac acc ttc 144

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe

15

20

25

act ccc tac tgg atg cag tgg gtg cga cag gcc cct gga caa ggg ctt 192

Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu

30

35

40

45

gag tgg atg gga tct att ttt cct gga gat ggt gat act agg tac agt 240

Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser

50

55

60

cag aag ttc aag ggc aga gtc acc atg acc gca gac aag tcc acg agc 288

Gln Lys Phe Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser

65

70

75

aca gcc tac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg 336

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val

80

85

90

tat tac tgt gcg aga gga tta cga cga ggg ggg tac tac ttt gac tac 384



Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr  
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 tgg ggg caa ggg acc acg gtc acc gtc tcc tca g 418  
 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
 110 115 120  
 <210> 14  
 <211> 418  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Nucleotide sequence coding for H chain V region version  
 s of humanized anti-HM 1.24 antibody  
 <400> 14  
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 Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly  
 -15 -10 -5  
 gct cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 96  
 Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 -1 1 5 10  
 cct ggg gcc tca gtg aag gtt tcc tgc aag gca tct gga tac acc ttc 144  
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 15 20 25  
 act ccc tac tgg atg cag tgg gtg cga cag gcc cct gga caa ggg ctt 192  
 Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
 30 35 40 45  
 gag tgg atg gga tct att ttt cct gga gat ggt gat act agg tac agt 240  
 Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser  
 50 55 60  
 cag aag ttc aag ggc aga gtc acc atc acc gca gac aag tcc acg agc 288  
 Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser  
 65 70 75  
 aca gcc tac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg 336

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 80 85 90  
 tat tac tgt gcg aga gga tta cga cga ggg ggg tac tac ttt gac tac 384  
 Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr  
 95 100 105  
 tgg ggg caa ggg acc acg gtc acc gtc tcc tca g 418  
 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
 110 115 120  
 <210> 15  
 <211> 1014  
 <212> DNA  
 <213> Homosapiens  
 <223> Nucleotide sequence coding for humam HM 1.24 antigenic  
 protein expressed on cell membrane  
 <400> 15  
 gaattcggca cgagggatct gg atg gca tct act tcg tat gac tat tgc 49  
 Met Ala Ser Thr Ser Tyr Asp Tyr Cys  
 1 5  
 aga gtg ccc atg gaa gac ggg gat aag cgc tgt aag ctt ctg ctg ggg 97  
 Arg Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly  
 10 15 20 25  
 ata gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg 145  
 Ile Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu  
 30 35 40  
 att atc ttc acc atc aag gcc aac agc gag gcc tgc cgg gac ggc ctt 193  
 Ile Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu  
 45 50 55  
 egg gca gtg atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag 241  
 Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu  
 60 65 70  
 ctg acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gcc gcc 289  
 Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala  
 75 80 85

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acc tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag      337
Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu
  90                      95                      100                      105
aag gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act      385
Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile thr
                      110                      115                      120
aca tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg      433
Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu
                      125                      130                      135
aga aga gaa aac cag gtc tta agc gtg aga atc gcg gac aag aag tac      481
Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr
                      140                      145                      150
tac ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg      529
Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala Pro Gln Leu Leu
                      155                      160                      165
att gtg ctg ctg ggc ctc agc gct ctg ctg cag tgagatccca ggaagctggc      582
Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln
                      170                      175                      180
acatcttggga aggtccgtcc tgctcggctt ttcgcttgaa cattcccttg atctcatcag      642
ttctgagcgg gtcattggggc aacacggtta gcggggagag cacggggtag ccggagaagg      702
gcctctggag caggtctgga ggggccatgg ggcagtcctg ggtgtgggga cacagtcggg      762
ttgaccacagg gctgtctccc tccagagcct ccctccggac aatgagtccc ccctcttgtc      822
tcccaccctg agattgggca tggggtgcgg tgtggggggc atgtgctgcc tgttgttatg      882
ggtttttttt gcgggggggg ttgctttttt ctggggtctt tgagctccaa aaaaataaac      942
acttcctttg agggagagca caccttaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaatc 1002
gggcggcgcg ca                                                    1014
<210> 16
<211> 132
<212> PRT
<213> Homosapiens
<223> Amino acid sequence of soluble HM 1.24 antigenic protein
<400> 16

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Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg  
1 5 10 15  
Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly  
20 25 30  
Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met  
35 40 45  
Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys  
50 55 60  
Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln  
65 70 75 80  
Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu  
85 90 95  
Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser  
100 105 110  
Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser  
115 120 125  
Ala Leu Leu Gln

130

<210> 17

<211> 115

<212> PRT

<213> Homosapiens

<223> Amino acid sequence of extra cellular downing of C-terminal lacking soluble HM 1.24 antigenic protein

<400> 17

Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg  
1 5 10 15  
Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly  
20 25 30  
Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met  
35 40 45  
Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys  
50 55 60

Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln  
 65 70 75 80  
 Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu  
 85 90 95  
 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser  
 100 105 110  
 Ser Ser Ala

115

&lt;210&gt; 18

&lt;211&gt; 143

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Amino acid sequence of a fusion protein comprising HA  
 peptide and soluble HM 1.24 antigenic protein

&lt;400&gt; 18

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys  
 1 5 10 15  
 Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu  
 20 25 30  
 Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu  
 35 40 45  
 Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser  
 50 55 60  
 Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu  
 65 70 75 80  
 Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu  
 85 90 95  
 Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala  
 100 105 110  
 Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala  
 115 120 125

Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln

130

135

140

<210> 19

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of a fusion protein comprising HA peptide and C-terminal lacking soluble HM 1.24 antigenic protein

<400> 19

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys

1

5

10

15

Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu

20

25

30

Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu

35

40

45

Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser

50

55

60

Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu

65

70

75

80

Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu

85

90

95

Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala

100

105

110

Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala

115

120

125

<210> 20

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of L chain V region version a of

humanized anti-HM 1.24 antibody

<400> 20

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Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
      -15              -10              -5
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
      -1   1              5              10
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val
      15              20              25
Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
      30              35              40              45
Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg
      50              55              60
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
      65              70              75
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser
      80              85              90
Thr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
      95              100             105

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<210> 21

<211> 139

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of H chain V region version r of  
humanized anti-HM 1.24 antibody

<400> 21

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Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly
      -15              -10              -5
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
      -1   1              5              10
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
      15              20              25

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Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
 30 35 40 45  
 Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser  
 50 55 60  
 Gln Lys Phe Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser  
 65 70 75  
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 80 85 90  
 Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr  
 95 100 105  
 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
 110 115 120

<210> 22

<211> 139

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of H chain V region version s of  
humanized anti-HM 1.24 antibody

<400> 22

Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly  
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 Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 -1 1 5 10  
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 15 20 25  
 Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
 30 35 40 45  
 Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser  
 50 55 60  
 Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser  
 65 70 75



Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
                   80                                  85                                  90

Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr  
           95                                  100                                  105

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
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<212> PRT

<213> Homosapiens

<223> Amino acid sequence of humam HM 1.24 antigenic protein  
 expressed on cell membrane

<400> 23

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Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu  
                                   20                                  25                                  30

Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala  
                                   35                                  40                                  45

Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg  
           50                                  55                                  60

Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly  
           65                                  70                                  75                                  80

Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met  
                                   85                                  90                                  95

Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys  
                                   100                                  105                                  110

Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln  
           115                                  120                                  125

Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu  
           130                                  135                                  140

Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser  
 145                                  150                                  155                                  160

Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser

165

170

175

Ala Leu Leu Gln

180